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BLASTP ALIGNMENT OF CEA-LIKE POLYPEPTIDE (SEQ ID NO: 3) WITH  
MOUSE CEA-RELATED CELL ADHESION MOLECULE 1 (SEQ ID NO: 12)

Query: CEA-like polypeptide (SEQ ID NO: 3)

Subject: gi|13937381 ref|NP\_036056.1| (NM\_011926) CEA-related cell  
adhesion molecule 1 (SEQ ID NO: 13); mouse hepatitis virus receptor;  
biliary glycoprotein carcinoembryonic antigen 7; carcinoembryonic antigen  
1 [Mus musculus] >emb|CAA47700.1| (X67283) biliary glycoprotein [Mus  
musculus]

Length = 341

Score = 204 (76.9 bits), Expect = 8.6e-16, P = 8.6e-16  
Identities = 54/168 (32%), Positives = 85/168 (50%)

Query: 73 RDKPVTVVQSIGTEVIGTLR----PDYRDRIRLFENGSLLLSDLQLADEGTYEVEISITD 128  
+ PV+ I V GT + P + R ++ NGSL+ + + D G Y +E+ TD  
Sbjct: 69 KGNPVSTNAEIVHFVTGTNKTTPAHSGRETIVSNGSLLIQRVTVKDTGVYTIEM--TD 126

Query:129 DTFTG-EKTINLTVDPISRQVLVASTTVLELSEAFNLNCSHENGTKPSYTWLKDGP 187  
+ F E T+ V P+++P + V +TTV EL ++ TL C N + WL + + L  
Sbjct:127 ENFRRTTEATVQFHVHQPVTQPSLQVTNTTVKEL-DSVTLTCL-SNDIGANIQWLFNSQSL 184

Query: 188 LND SRMLLSPDQKVLITITRVLMEDEDDLYSCMVENPISQGRSLPVKITV 235  
RM LS + +L I + ED Y C + NP+S RS +K+ +  
Sbjct: ,185 QLTERMTLSQNN SILRIDPIKREDAGEYQCEISNPVSVKRSNSIKLDI 232

FIG. 1

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**BLASTP ALIGNMENT OF CEA-LIKE POLYPEPTIDE (SEQ ID NO: 8) WITH  
MOUSE PROTEIN SIMILAR TO CEA-RELATED CELL ADHESION MOLECULE 6  
PRECURSOR (SEQ ID NO: 14)**

Query: CEA-like polypeptide (SEQ ID NO: 8)

Subject: gi|20841606 ref|XP\_133045.1| (XM\_133045) similar to  
Carcinoembryonic antigen-related cell adhesion molecule 6 precursor (SEQ  
ID NO: 14) (Normal cross-reacting antigen) (Nonspecific crossreacting  
antigen) (CD66c antigen) [Mus musculus]

Length = 463

Score = 284 (105.0 bits), Expect = 1.2e-22, P = 1.2e-22  
Identities = 77/236 (32%), Positives = 121/236 (51%)

```
Query:      8 LSRASRALRLAPFVYLLLIQTDPLEGVNITSPVRLIHGTVGKSALLSVQYS--STSSDRP 65
              L R+   L L   ++LLLI   L G+ +T P   +HG  G++  L V Y   + +SD
Sbjct:      9 LLRSMVGLSLCK-IHLLLIAGSCL-GLKVTVPSTYTVHGIRGQALYLPVHYGFHTPASDIQ 66

Query: 66 VVKWQLKRDK--PVTVVQSIGTEVIGTLRPDYRDRIRLFE-NGSLLLSDLQLADEGTYEV 122
              ++ W  +R   P  ++ S+   V+  L  +Y+ +  +  N SLL++ LQ  DEG Y V
Sbjct: 67 II-WLFERSHTMPKYLLGSVNKSVPDL--EYQHKFTMMPPNASLLINPLQFTDEGNYIV 123

Query:123 EISITDD-TFTGEKTINLTVDPISRPQVLV-ASTTVLELSEAF TLNCSHENGTKPSYTW 180
              +++I  + T +  + I +TVD P+ +P V   ++  +E      TL C  E GT+  Y W
Sbjct:124 KVN IQNGTLSASQKIQVTVD PVMKPMVQFHPASGAVEYVGNITLTCQVEGGTRLVYQW 183

Query:      181 LKDGKPLLND SRMLLSPDQKVLITITRVLME DDDLYSCMVENPISQGRSLPVKITVY 236
              K GKP+  +S   SP   L I  V  ED   Y+C+V NP+S+  S  +  T+Y
Sbjct:      184 RKSGKPISINSSHSFSPQNNTLWIVPVTKEDIGNYTCLVSNPVSEMESDIIMPTIY 239
```

**FIG. 2**

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CLUSTALW MULTIPLE SEQUENCE ALIGNMENT BETWEEN CEA-LIKE  
POLYPEPTIDES OF THE INVENTION (SEQ ID NO: 4 AND 9)

```

SEQ 4   MKRREGALSRSRALRLAPFVYLLLIQTDPLEGVNITSPVRLIHGTVGKSALLSVQYSST
SEQ 9   MKRREGALSRSRALRLAPFVYLLLIQTDPLEGVNITSPVRLIHGTVGKSALLSVQYSST
*****

SEQ 4   SSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRPDYRDRIRLFENGSLLLSDLQLADEGTY
SEQ 9   SSDRPVVKWQLKRDKPVTVVQSIGTEVIGTLRPDYRDRIRLFENGSLLLSDLQLADEGTY
*****

SEQ 4   EVEISITDDTFTGEKTINLTVDPISRPQVLVASTTVLELSEAFTLNCSHENGTKPSYTW
SEQ 9   EVEISITDDTFTGEKTINLTVDPISRPQVLVASTTVLELSEAFTLNCSHENGTKPSYTW
*****

SEQ 4   LKDGKPLLND SRMLLSPDQKVL TITRVL MEDDDLYSCMVENPISQGRSLPVKITVYRRSS
SEQ 9   LKDGKPLLND SRMLLSPDQKVL TITRVL MEDDDLYSCMVENPISQGRSLPVKITVYRRSS
***** **:*****.***:** *****: **

SEQ 4   LYIILSTGGIFLLVTLVTV CACWKPSKR-----SG
SEQ 9   LYIILSTGGIFLLVTLVTV CACWKPSKRKQKKLEKQNSLEYMDQNDDR LKPEADTLPRSG
***** **

SEQ 4   -----
SEQ 9   EQERKNPMALYILKDKDSPETEENPAPEPR SATEPGPPGYSVSPA VPGRSPGLPIRSARR

SEQ 4   -----
SEQ 9   YPRSPARSPATGRTHSSPPRAPSSPGRSRSASRTLRTAGVHI IREQDEAGPVEISA

```

FIG. 3

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MULTIPLE SEQUENCE ALIGNMENT BETWEEN CHEMOKINE-LIKE  
POLYPEPTIDES (SEQ ID NO: 18, 22, 26, 30, AND 34 AND CHEMOKINES  
MCP-3 AND MIP-1a (SEQ ID NO: 41 AND 42)

```

SEQ 14      MQLLKAL-WALAGAALCCFLVLVIHAQFLKEGQL-----AAGT-CEIVTLDR
SEQ 10      MSERVERNWTGGWLLALCL--AWLWTHLTLAALQPP-----TATVLVQQGT-CEVIAAHR
SEQ 6       MSKRYLQKATKGK-LL- -III-FIVTLWGKVVSSANHHK-----AHHVKTGT-CEVVALHR
SEQ 18      MRSPRMRVCAKSV-LLSHWLFLAYVLMVCKLMSASSQHLRGHAGHHQIKQGT-CEVVAVHR
SEQ 2       M--AMV--SAMSWVLYLWISACAMLLCHGSLQHTFQQHH-----LHRPEGGT-CEVIAAHR
MCP-3       M-KASAA-----LLCLLLTAAAFSPQGLAQPVG-----INTS-T-T-----
MIP-1a      MQVSTAALAV---LLCTM---ALCNQFSASLAAD-----TPTA-----
              **           :                       ** :

SEQ 14      DS----SQPRR-----TIA-R-QTAR-CACRKGQIAG-TTRARPACVDARI--IKTKQWCDML
SEQ 10      CC----NRNRI-----EE--RSQTVK-CSCFSGQVAG-TTRAKPSCVDASI--VLQRWWCQME
SEQ 6       CC----NKNKI-----EE--RSQTVK-CSCFPGQVAG-TTRAAPSCVDASI--VEQKWWCHMQ
SEQ 18      CC----NKNRI-----EE--RSQTVK-CSCFPGQVAG-TTRAQPSCVEASI--VIQKWWCHMN
SEQ 2       CC----NKNRI-----EE--RSQTVK-CSCLPGKVAG-TTRNRPSCVDASI--VIGKWWCEME
MCP-3       CCYRFINK-KIPKQRL-ESYRRTTSSHCPRE-A-VIFKTKLDKEICADPTQKWV-QDF---MK
MIP-1a      CCFSYTSR-QIPQNFIADYFE--TSSQCSK-PG-VIFLTKRSRQVCADPSEEWV-QKYV-SD
              **      : : . *      : . * . *      : * : : *      * : : : :

SEQ 14      PCLEGECDLLINRSGWTCTQPGGRIKTTTVS---
SEQ 10      PCLPGEECKVLPDLSGWSCSS-GHKVKTTKVTR--
SEQ 6       PCLEGECKVLPDRKGWSCSS-GNKVKTTTRVTH--
SEQ 18      PCLEGEDCKVLPDYSGWSCSS-GNKVKTTKVTR--
SEQ 2       PCLEGECKTLPDMSGWMCAT-GNKIKTTTRHPRT
MCP-3       H-LDKK--TQTPKL-----
MIP-1a      LELSA-----
              *

```

FIG. 4

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BLASTP ALIGNMENT OF ADIPONECTIN-LIKE POLYPEPTIDE (SEQ ID NO:  
44) WITH ADIPONECTIN/APM1 (SEQ ID NO: 55)

29.6% identity;

Global alignment score: 399

```

      10      20      30      40      50
SEQ 44  MALGLLIAVPLLLQAAPRGAAHYEMMGTCRMICDPYTAAPGGEPPGAKAQP----PGPST
      . . . . .
SEQ 55  -----MLLLGAVLLL---LALPGHDQETTTQGPVLLPLPKG
              10              20              30

      60      70      80      90      100      110
SEQ 44  AALEVMQDLSANPPPPFIQGPKGDPGRPGKPGPRGPPGEPGPPGPRGPPGEGKDSGRPGL
      : : . . . : : : : : : : : : : : : : : : : : : :
SEQ 55  ACTGWMAGIPGHP-----GHNGAPGRDGRDGTPEKGEKGDPLIGPKGDIGETGVPGA
              40              50              60              70              80

      120      130      140      150      160      170
SEQ 44  PGLQLTAGTASGVGVVGGGAGVGGDSEGEVTSALSATFSGPKIAFYVGLKSPHEGYEV-L
      : . : . : : : : : : : : : : : : : : : : :
SEQ 55  EGPRGFPGIQGRKGEPGEGAYVY-----RSAFSVGLETYVTIPNMPI
      90      100      110              120      130

      180      190      200      210      220      230
SEQ 44  KFDDVVTNLGNHYDPTTGKFSCQVRGIYFFTYHILMRGGDGTSMWADLCKNGQVRASAIA
      . : . : : : : : : : : : : : : : : : : : .
SEQ 55  RFTKIFYNQNHVDGSTGKFHCNIPGLYYFAYHITVYMKD---VKVSLFKKDKAMLFTYD
              140      150      160      170      180

      240      250      260      270      280
SEQ 44  QDADQNYDYASNSVVLHLDGDEVYVKLDG-GKAHG--GNNNKYSTFSGFLLYPD--
      : . : : : : : : : : : : : : : : : : : : : :
SEQ 55  QYQENNVDQASGSVLLHLEVGDQVWLQVYGEGERNGLYADNDNDSTFTGFLLYHDTN
      190      200      210      220      230      240
```

FIG. 5

**FIG. 6**

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MODULAR STRUCTURES OF ADIPONECTIN (SEQ ID NO: 55) AND  
ADIPONECTIN-LIKE PROTEIN (SEQ ID NO 44)

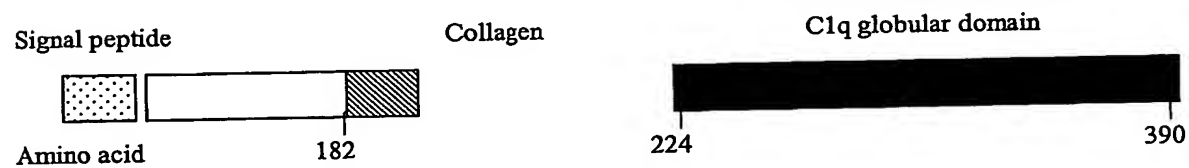


FIG. 7

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BLASTP ALIGNMENT OF ADIPONECTIN-LIKE POLYPEPTIDE (SEQ ID NO:  
50) WITH ADIPONECTIN/APM1 (SEQ ID NO: 55)

21.8% identity; Global alignment score: 398

```

      10      20      30      40      50      60
SEQ 50  MSKGMCPCLAVAGLGVEAECTMITAKCRHQAFGYTSFTQTRASHFLVEEKDPRSRS
SEQ 55  -----

      70      80      90     100     110     120
SEQ 50  PSAGAGRPRRPTITSPGGKEELVAVASRLWQRRRRACLAAVGVLLAMALGLLIAVPLLLQ
SEQ 55  -----

      130     140     150     160     170
SEQ 50  AAPRGAHYEMMGTCRMICDPYTAAPGGEPPGAKAQP----PGPSTAALVEMQDLSANPP
      . . . . . : : : : : : : : : : : : : : : : : :
SEQ 55  -----MLLLGAVLLL-----LALPGHDQETTTQGPVLLPLPKGACTGWMAGIPGHP-
      10      20      30      40

      180     190     200     210     220     230
SEQ 50  PPFIQGPKGDPGRPGKPGPRGTTGEPGPPGPRGPPGEGKDSGRPGLPGLRLTAGSASGVG
      : : : : : : : : : : : : : : : : : : : : : : :
SEQ 55  -----GHNGAPGRDGRDGTTPGEKGEKGDPLIGPKGDIGETGVPGAEGPRGFPPIQGRKG
      50      60      70      80      90     100

      240     250     260     270     280     290
SEQ 50  VVARGAGVGGDSEGEVTSALSATFSGPKIAFYVGLKSPHEGYEV-LKFDDVVTNLGNHYD
      . . . : : : : : : : : : : : : : : : : : :
SEQ 55  EPGEGAYVY-----RSAFSVGLETYVTIPNMPPIRFTKIFYNQQNHYD
      110     120     130     140

      300     310     320     330     340     350
SEQ 50  PTTGKFSCQVRGIYFFTYHILMRGGDGTSMWADLCKNGQVRASAIQDADQNYDYASNSV
      . . . : : : : : : : : : : : : : : : : : :
SEQ 55  GSTGKFHCNIPGLYYFAYHITVYMKD---VKVSLFKKDKAMLFTYDQYQENNVDQASGSV
      150     160     170     180     190     200

      360     370     380     390
```



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BLASTP ALIGNMENT OF ADIPONECTIN-LIKE POLYPEPTIDE (SEQ ID NO:  
50) WITH C1q-RELATED FACTOR (SEQ ID NO: 54)

45.1% identity; Global alignment score: 1217

```

      10      20      30      40      50      60
SEQ 50  MSKGMCPICICLAVAGLGVEAECTMITAKCRHQAFGYTSFTQTRASHFLVEEKDPRSRS
SEQ 54  -----

      70      80      90     100     110     120
SEQ 50  PSAGAGRPRRPTITSPGGKEELVAVASRLWQRRRRACLAAGVLLAMALGLLIAVPLLLQ
      : : : . . . . .
SEQ 54  -----MLLVLVVLIPLVLS
                        10

     130     140     150     160     170
SEQ 50  AA-PRGAAHYEMMGTCRMICDPYTAAPGGEPPGAKAQPPGPSTAALEVMQDLSANPPPP-
      . . : : : : : : : : : . : : : . : : : :
SEQ 54  SGGPEG--HYEMLGTCRMVCDPYPA----RGPGAGARTDGG-----DALSEQSGAPPPST
      20      30      40      50      60

    180     190     200     210     220     230
SEQ 50  FIQGPKGDPGRPGKPGPRGTTGEPGPPGPRGPPGEKGDSEGRPGLPGLRLTAGSASGVGVV
      . . . . : : : : : : : : : : : : : : : : : : : :
SEQ 54  LVQGPQGKPGRTGKPGPPGPPGDPGPPGPGVGPGEKGEPPGKPGPPGL-----
      70      80      90     100     110

    240     250     260     270     280     290
SEQ 50  ARGAGVGGDSEGEVTSALSATFSGPKIAFYVGLKSPHEGYEVLKFDDVVTNLGNHYDPTT
      : : : : : : : : : : : : : : : : : : : : : :
SEQ 54  ---PGAGGS--GAISTATYTTV--PRVAFYAGLKNPHEGYEVLKFDDVVTNLGNHYDAAS
      120     130     140     150     160

    300     310     320     330     340     350
SEQ 50  GKFSCQVRGIYFFTYHILMRGGDGTSMWADLCKNGQVRASAIQDADQNYDYASNSVVLH
      . . . . : : : : : : : : : : : : : : : : : :
SEQ 54  GKFTCNIPGTYFFTYHVLMRGGDGTSMWADLCKNGQVRASAIQDADQNYDYASNSVILH
      170     180     190     200     210     220

    360     370     380     390
```

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CLUSTALW MULTIPLE SEQUENCE ALIGNMENT BETWEEN ADIPONECTIN-LIKE  
POLYPEPTIDES OF THE INVENTION (SEQ ID NO: 44 AND 50)

CLUSTAL W (1.83) multiple sequence alignment

```
SEQ 50      MSKGMCPICICLAVAGLGVEAECTMITAKCRHQAFGFYTSFTQRTTRASHFLVEEKDPRSRS
SEQ 44      -----

SEQ 50      PSAGAGRPRRPTITSPGGKEELVAVASRLWQRRRRACLAAGVLLAMALGLLIAVPLLLQ
SEQ 44      -----MALGLLIAVPLLLQ
                      *****

SEQ 50      AAPRGAAHYEMMGTCRMI CDPYTAAPGGEPPGAKAQPPGPSTAALVMDLSANPPPPFI
SEQ 44      AAPRGAAHYEMMGTCRMI CDPYTAAPGGEPPGAKAQPPGPSTAALVMDLSANPPPPFI
                      *****

SEQ 50      QGPKGDPGRPGKPGPRGTTGEPGPPGPRGPPGEKGDSCRPGLPGLRLTAGSASGVGVVAR
SEQ 44      QGPKGDPGRPGKPGPRGPPGEPGPPGPRGPPGEKGDSCRPGLPGLQLTAGTASGVGVVGG
                      *****:****:*****.

SEQ 50      GAGVGGDSEGEVTSALSATFSGPKIAFYVGLKSPHEGYEVLKFDDVVTNLGNHYDPTTGK
SEQ 44      GAGVGGDSEGEVTSALSATFSGPKIAFYVGLKSPHEGYEVLKFDDVVTNLGNHYDPTTGK
                      *****

SEQ 50      FSCQVRGIYFFTYHILMRGGDGTSMWADLCKNGQVRASAI AQDADQNYDYASNSVVLHLD
SEQ 44      FSCQVRGIYFFTYHILMRGGDGTSMWADLCKNGQVRASAI AQDADQNYDYASNSVVLHLD
                      *****

SEQ 50      SGDEVYVKLDGGKAHGGNNNNKYSTFSGFLLYPD
SEQ 44      SGDEVYVKLDGGKAHGGNNNNKYSTFSGFLLYPD
                      *****
```

FIG. 10

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CLUSTAL W MULTIPLE SEQUENCE ALIGNMENT OF LY-6-LIKE  
POLYPEPTIDES (SEQ ID NO: 58, 65, AND 71) WITH HUMAN "EXPRESSED  
IN PROSTATE AND TESTIS" (PATE) SEQ ID NO: 103

```

SEQ 58  MNKHFLFLF-LLYCLIVAVTS-----L-----QCITCHLRTRTDRC 35
SEQ 65  MDKSLLELPIILLCCFRALSGSLSMRNDVNEIVAVKNNFPVIEIVQCRMCHLQFPGEKC 60
SEQ 71  MDKSLLELPIILLCCFRALSGSLSMRNDV--I-----EIVQCRMCHLQFPGEKC 48
SEQ 103 MDKSLLELPIILLCCFRALSGSLSMRNDVNEIVAVKNNFPVIEIVQCRMCHLQFPGEKC 60
      *: * : * : : * * : * : . : * * * : : *

SEQ 58  RRGFGVCTAQKGEACMLLRIVQRN-TLQISYMCQKFCRDMTFDLNRNRTYVHT-CCN-YN 92
SEQ 65  SRGRGICTATTEEACMVGRMFKRDNPNWLTFTMGCLKNCADVKGIRWSVYLVNFRCCRSHD 120
SEQ 71  SRGRGICTATTEEACMVGRMFKRDNPNWLTFTMGCLKNCADVKGIRWSVYLVNFRCCRSHD 108
SEQ 103 SRGRGICTATTEEACMVGRMFKRDNPNWLTFTMGCLKNCADVKGIRWSVYLVNFRCCRSHD 120
      ** *:*** . ****: *::*: . :::* * * * *: . * : ** . :

SEQ 58  YCNFKL 98
SEQ 65  LCNEDL 126
SEQ 71  LCNEDL 114
SEQ 103 LCNEDL 126
      ** . *

```

FIG. 11

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CLUSTAL W MULTIPLE SEQUENCE ALIGNMENT OF LY-6-LIKE  
POLYPEPTIDES (SEQ ID NO: 78, 83, AND 90) WITH HUMAN SP-10 (SEQ  
ID NO: 104)

```

SEQ 83      MNRFLLLSLYLLGSARGTSSQPNELSGSIDHQTSVQQLPGEQPSGEQPSGEHLSGEQPL 60
SEQ 78      MNRFLLLSLYLLGSARGTSSQPNELSGSIDHQTSVQQLPGEQPSGEQPSGEHLSGEQPL 60
SEQ 90      MNRFLLLSLYLLGSARGTSSQPNELSGSIDHQTSVQQLPGEQPSGEQPSGEHLSGEQPL 60
SEQ 104     MNRFLLLSLYLLGSARGTSSQPNELSGSIDHQTSVQQLPGEQPSGEQPSGEHLSGEQPL 60
            *****

SEQ 83      SELESGEQPSDEQPSGEHGSGEQPSGEQASGEQPSG----- 96
SEQ 78      SELESGEQPSDEQPSGEHGSGEQPSGEQASGEQPSG-----TILNC 101
SEQ 90      SELESGEQPSDEQPSGEHGSGEQPSGEQASGEQPSGEHASGEQASGAPISSTSTGTILNC 120
SEQ 104     SELESGEQPSDEQPSGEHGSGEQPSGEQASGEQPSGEHASGEQASGAPISSTSTGTILNC 120
            *****

SEQ 83      --EHASGE-----QASGAPISSTS-----TGGKLQFMVQGCENMCPSMNLFSHGTR 140
SEQ 78      YTCAYMNDQGKCLRGEGETCITQNSQQCMLKKIFEGGKLQFMVQGCENMCPSMNLFSHGTR 161
SEQ 90      YTCAYMNDQGKCLRGEGETCITQNSQQCMLKKIFEGGKLQFMVQGCENMCPSMNLFSHGTR 180
SEQ 104     YTCAYMNDQGKCLRGEGETCITQNSQQCMLKKIFEGGKLQFMVQGCENMCPSMNLFSHGTR 180
            .:      :...*: *...*      *****

SEQ 23      MQIICCRNQSFCKNI 155
SEQ 28      MQIICCRNQSFCKNI 176
SEQ 35      MQIICCRNQSFCKNI 195
SEQ 49      MQIICCRNQSFCKNI 195
            *****

```

FIG. 12

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CLUSTAL W MULTIPLE SEQUENCE ALIGNMENT OF LY-6-LIKE POLYPEPTIDE  
(SEQ ID NO: 97) WITH MURINE "SIMILAR TO LY-6H" PROTEIN(SEQ ID  
NO: 105)

```

SEQ 97      MERLVLTLCCTLPLAVASAG---CATTPARNLSCYQCFKVSSWTECPPTWCSPLDQVCISN 57
SEQ 105     MAPLLLLVLWASLVSMELTGGMMVNEVPAQNLSCFECFKVLQASKCHPIECPNEKVCVSN 60
          *  *:*. *  :   ::  :*          .**:*:**:*:**.  .  ::* *  * *  :*:**

SEQ 97      EVVVSFKWSVRVLLSKRCAPRCPNNDNMKFEWSPAPMVQGVITRRCCSWALCNRALTPQEG 117
SEQ 1-5     EVLLYTSTKRRTQISKRCATACPNNSNNVIEWDPS-FFQ--ISV-----QSS 103
          **::  .  .  *.  :*****.  ***.*  :**.*:  :.*  *:          *..

SEQ 97      RWALRGGLLLQDPSRGRRTWVRPQLGLPLCLPISSPLCPRETQEG 162
SEQ 105     --MTRASKISMEPS--K-----QE-----TDSYTOHRAVPEA 131
          *..  :  :**  :          *          .*  *  .  *.

```

FIG. 13

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CLUSTAL W MULTIPLE SEQUENCE ALIGNMENT OF THE uPAR/LY-6 DOMAINS  
OF LY-6-LIKE POLYPEPTIDES WITH uPAR/LY-6 DOMAINS OF HUMAN uPAR  
(SEQ ID NO: 102), PATE (SEQ ID NO: 103) AND SP-10 (SEQ ID NO:  
104)

```

SEQ 62  LQCITCHL-RTRTDCRRGFGV---CTAQKGEACMLLRITYQ-----RNTLQISYMVC--QK 70
SEQ 69  VQCRMCHL-QFPGEKCSRGRGI---CTATTEEACMVGRMFKR-----DGNPWLTFFMGC--LK 84
SEQ 75  VQCRMCHL-QFPGEKCSRGRGI---CTATTEEACMVGRMFKR-----DGNPWLTFFMGC--LK 84
SEQ 87  LNCYTCAY-MNDQGKCLRGEET---CITQNSQQCMLKKIFE-----GGKLQFMVQGC--EN 148
SEQ 94  LNCYTCAY-MNDQGKCLRGEET---CITQNSQQCMLKKIFE-----GGKLQFMVQGC--EN 167
SEQ 101 LSCYQCFK-VSSWTECPPTW----CSPLDQV-CISNEVVVSFK---WSVRVLLSKRC--AP 77
PATE    VQCRMCHL-QFPGEKCSRGRGI---CTATTEEACMVGRMFKR-----DGNPWLTFFMGC--LK 96
SP-10   LNCYTCAY-MNDQGKCLRGEET---CITQNSQQCMLKKIFE-----GGKLQFMVQGC--EN 167
uPAR d1 LRCMQCKT--NG--DCRVEE----CALGQDL-CRTTIVRLWEE---GEELELVEKSC--TH 47
uPAR d2 LECISCGS-SDMS--CERGRHQSLQCRSPPEEQ-CLDVVTHWIEGEEGRPKDDRHLRGCGYLP 151
uPAR d3 RQCYSCKGNSTHG--CSSEETFLIDCRGPMNQ-CLVATGTHE-----PKNQSYMVRGCATAS 245
      *  *  *      *      *      *

```

```

SEQ 62  FCRDMTF-DLRN----RTYVHT-CC-NYNYCNFKL 98
SEQ 69  NCADVKG-IRWS-----VYLVNFRCCRSHDLCNEDL 114
SEQ 75  NCADVKG-IRWS-----VYLVNFRCCRSHDLCNEDL 114
SEQ 87  MCPSMN--LFSH----GTRMQIICCRNQSFCKNI- 176
SEQ 94  MCPSMN--LFSH----GTRMQIICCRNQSFCKNI- 195
SEQ 101 RCPNDNMKFEWSPAPMVQGVITRRCC-SWALCNRAL 112
PATE    NCADVKG-IRWS-----VYLVNFRCCRSHDLCNEDL 126
SP-10   MCPSMN--LFSH----GTRMQIICCRNQSFCKNI- 195
uPAR d1 SEKTNRTLSYRTG--LKITSLTEVVC-GLDLCNQGN 80
uPAR d2 GCPGSNG-FHNN-----DTFHFLKCC-NTTKCNEGP 180
uPAR d3 MCQHAHLGDAFS-----MNHIDVSCC-TKSGCNHPD 275

```

FIG. 14

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CONSENSUS SEQUENCE OF THE uPAR/LY-6 CYSTEINE-RICH DOMAIN THAT  
DEFINES THE LY-6 SUPERFAMILY

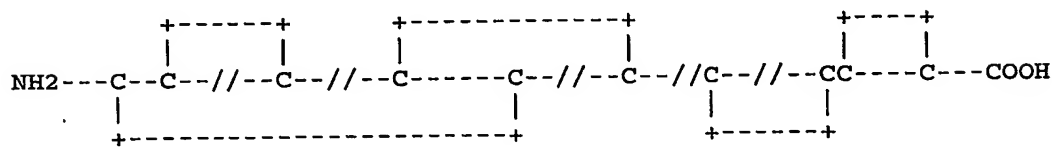


FIG. 15

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SCHEMATIC DIAGRAM OF STRUCTURAL FEATURES OF THE LY-6-LIKE  
POLYPEPTIDES OF THE INVENTION

SEQ ID NO: 3



SEQ ID NO: 10



SEQ ID NO: 42



SEQ ID NO: 35

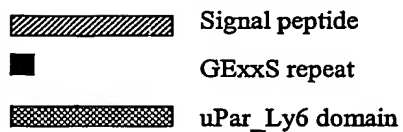
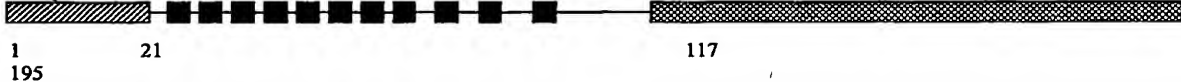


FIG. 16